RAW SEQUENCE LISTING DATE: 06/12/2003
PATENT APPLICATION: **US/09/765,061D** TIME: 09:02:28

Input Set : **A:\UTHou-16UTL 79-88.ST25.txt**
Output Set: **N:\CRF4\06122003\I765061D.raw**

Does Not Comply
Corrected Diskette Needed

invalid, per 1.825 of Sequence Rules.

A sequence listing must begin with sequence 1

insert sequences 1-78 from previously submitted CRF.

"Any amendment to the paper copy of the Sequence Listing... must be accompanied by a substitute copy of the computer readable form... including all previously submitted data..."

```
 3 <110> APPLICANT: The Board of Regents of the University of Texas System
 5 <120> TITLE OF INVENTION: MUTATIONS IN A NOVEL PHOTORECEPTOR-PINEAL GENE ON 17P CAUSE
LEBER
 6       CONGENITAL AMAUROSIS (LCA4)
 8 <130> FILE REFERENCE: 96606/16UTL
10 <140> CURRENT APPLICATION NUMBER: 09/765,061D
11 <141> CURRENT FILING DATE: 2001-01-17
13 <150> PRIOR APPLICATION NUMBER: 60/331362
14 <151> PRIOR FILING DATE: 2001-01-04
16 <160> NUMBER OF SEQ ID NOS: 10 additional sequences, Seq. Nos. 79-88
18 <170> SOFTWARE: PatentIn version 3.2
20 <210> SEQ ID NO: 79
21 <211> LENGTH: 34
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
26 <220> FEATURE:
27 <221> NAME/KEY: misc_feature
28 <222> LOCATION: (1)..(34)
29 <223> OTHER INFORMATION: Donor Splice Site: Residue 1-10 are the exonic sequence and
30       Residues 11-34 are the intronic sequence
32 <400> SEQUENCE: 79
33 cggatcccga gtgagtgggg ccctccggag caga                                    34
36 <210> SEQ ID NO: 80
37 <211> LENGTH: 35
38 <212> TYPE: DNA
39 <213> ORGANISM: Homo sapiens
42 <220> FEATURE:
43 <221> NAME/KEY: misc_feature
44 <222> LOCATION: (1)..(35)
45 <223> OTHER INFORMATION: Acceptor Splice Site: Residues 1-25 are the intronic sequence
46       and Residues 26-35 are the exonic sequence.
48 <400> SEQUENCE: 80
49 cagagtgcac cgtctcggtg actaggtgat ctttc                                   35
52 <210> SEQ ID NO: 81
53 <211> LENGTH: 35
54 <212> TYPE: DNA
55 <213> ORGANISM: Homo sapiens
58 <220> FEATURE:
59 <221> NAME/KEY: misc_feature
60 <222> LOCATION: (1)..(35)
61 <223> OTHER INFORMATION: Donor Splice Site: Residue 1-10 are the exonic sequence and
62       Residues 11-35 are the intronic sequence
64 <400> SEQUENCE: 81
65 csacaccatc gtaagtaggc cctgcgcgcc tgtct                                   35
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<210> SEQ ID NO: 82
<211> LENGTH: 35
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(35)
<223> OTHER INFORMATION: Acceptor Splice Site: Residues 1-25 are the intronic sequence and Residues 26-35 are the exonic sequence.
<400> SEQUENCE: 82
gccatccatc cgtttatccc cacagcacac ggggg 35
<210> SEQ ID NO: 83
<211> LENGTH: 35
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(35)
<223> OTHER INFORMATION: Donor Splice Site: Residue 1-10 are the exonic sequence and Residues 11-35 are the intronic sequence
<400> SEQUENCE: 83
gctgctgcag gtggggctgg ggttggcagg gctgg 35
<210> SEQ ID NO: 84
<211> LENGTH: 35
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(35)
<223> OTHER INFORMATION: Acceptor Splice Site: Residues 1-25 are the intronic sequence and Residues 26-35 are the exonic sequence.
<400> SEQUENCE: 84
cactgacctg cagctctggg gccaggttga tgccc 35
<210> SEQ ID NO: 85
<211> LENGTH: 35
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(35)
<223> OTHER INFORMATION: Donor Splice Site: Residue 1-10 are the exonic sequence and Residues 11-35 are the intronic sequence
<400> SEQUENCE: 85
gcagaccaag gtcagaggcc gctggccacg gggtg 35
<210> SEQ ID NO: 86
<211> LENGTH: 35
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:

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     139 <221> NAME/KEY: misc_feature
     140 <222> LOCATION: (1)..(35)
     141 <223> OTHER INFORMATION: Acceptor Splice Site: Residues 1-25 are the intronic
sequence
     142       and Residues 26-35 are the exonic sequence.
     144 <400> SEQUENCE: 86
     145 catggctgac cttctccctg ggcaggagaa gccrt                                  35
     148 <210> SEQ ID NO: 87
     149 <211> LENGTH: 35
     150 <212> TYPE: DNA
     151 <213> ORGANISM: Homo sapiens
     154 <220> FEATURE:
     155 <221> NAME/KEY: misc_feature
     156 <222> LOCATION: (1)..(35)
     157 <223> OTHER INFORMATION: Donor Splice Site: Residue 1-10 are the exonic sequence and
     158       Residues 11-35 are the intronic sequence
     160 <400> SEQUENCE: 87
     161 caccacccag gtgcgcgggg ctgcaggggc ggaca                                  35
     164 <210> SEQ ID NO: 88
     165 <211> LENGTH: 35
     166 <212> TYPE: DNA
     167 <213> ORGANISM: Homo sapiens
     170 <220> FEATURE:
     171 <221> NAME/KEY: misc_feature
     172 <222> LOCATION: (1)..(35)
     173 <223> OTHER INFORMATION: Acceptor Splice Site: Residues 1-25 are the intronic
sequence
     174       and Residues 26-35 are the exonic sequence.
     176 <400> SEQUENCE: 88
     177 gctggatgct ccctgctccc cacaggcatc gtgaa                                   35
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VERIFICATION SUMMARY DATE: 06/12/2003
PATENT APPLICATION: **US/09/765,061D** TIME: 09:02:29

Input Set : **A:\UTHou-16UTL 79-88.ST25.txt**
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